Takeshima, K.

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alignment_block:
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                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
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        101
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                                                                                                                 1 MetThrArgSerProProLeuArgGluLeuProProSerTyrThrProPr 17
oAlaArgThrAlaAlaProGlnIleLeuAlaGlySerLeuLysAlaProL 34
                                                                                                     ATGGTTCGGCCACTGTCCCTTGGAGAGCTACCTCCCAGCTACACACCTCC 50
                                                  ACTCGGTCCTCCGCACCTCATATCCTAGCTGGGAGCCTGCAGGCTCCTC 100
                                                                                                                                                                                                                         Quality: 5420.00
Ratio: 4.892
milarity: 97.023
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                                                                                                                                                                                                                                                                                                                            PTLPQSFARVTTSMTVALHPPPLPGAYVHPASEEPT"
                                                                                                                                                                                                                                                                                                                                     EFTVHVALGFLTSHGSRNLRAASALEQTFAPVTDGAVSTLLJILMLAGSNFDFIIRYF
FVVLTVLTLLGLLHGLLLLFVLLSILGPPPQVVQVYKESPQTLNSAAPQRGGLRWDRP
                                                                                                                                                                                                                                                                                                                                                               VCTFLVCALLLLSPWTAGLIVLVLAMMTVELFGIMGFLGIKLSAIPVVILVASIGIGV
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1. .3549
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                                                                                                                                                                                                                                                                                          251 ProCysLeuHisProAspAspLeuHisCysProProSerAlaProAsnHi
                                                                                                                                                                                                                                                                                                                                    701
                                                                                                                                                                                                                                                                                                                                           234 heArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 LysGluLysLeuGlyGluGluAlaAlaTyrThrSerGlnMetLeuIleGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AGCTCTGGGTAGAAGTGGGCAGCAGGGTGAGCCAGGAGCTGCACTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
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                                                                                                                                                                                                                             GCACAGCAGGCAGGCTCCCAATGTGGCTCAGGAGCTGAGTGGGGGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATCCTCACCCCGCTTGACTGCTTCTGGGAAGGAGCCAAACTCCAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ulleGluAsnGlyMetIleGluArgMetIleGluLysLeuPheProCysV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGCTTCTCCCACAAGTTCATGCACTGGCAGGAAGGAACTGCTACTAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTGCGCACCAGGAAGGGGGAAACGTCCTCACCCCCGAGGCACTTGACT 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nThrAlaArgGlnGluGlyGluAsnIleLeuThrProGluAlaLeuGlyL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGAGAAGCTGGGGGAAGAGGCTGCGTACACCTCCCAGATGTTGATTCA
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 seq_documentation_block:
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Patent No. 6348575
   GENERAL INFORMATION:
   GEMERAL INFORMATION:
APPLICANT: de Sauvage, Frederic
APPLICANT: Carpenter, David A.
TITLE OF INVENTION: Patched-2
FILE REFERENCE: P1405R1
CURRENT APPLICATION NUMBER: US/09/293,505
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 60/081,884
EARLIER FILING DATE: 1998-04-15
NUMBER OF SEO ID NOS: 32
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     TYPE: DNA
     ORGANISM: Homo sapiens
US-09-293-505-1
alignment_scores:
Quality: 5911.00
Ratio: 5.185
Percent Similarity: 99.825
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US-09-807-007-1 x US-09-293-505-1
Align seg 1/1 to: US-09-293-505-1 from: 1 to: 4030
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GINTUYSSETTPANSPLEUNASILYSIIECYSTYTLYSSETGLYVALPTOLE GGGAAGTCCTGGGATTGAACAAACTCGCTACAAGTCAGAGTTCCCCTT ULleGluAsnGlyMetIleGluArgmetIleGluLysLeubheProcysy	43	41	40	388	33	28	23	18	30	28	03	oo iii	ຕ ຕ	a i	w o	œ œ	ω is	ao in	
	34 laLeuAlaValAlaSerGlyLeuGlyLeuCysAlaLeuLeuGlyIleThr 	17 pCysalaGlnSerGlnGlySerValGlyLeuAlaGlyValLeuLeuValA	01 GlyTyrLeuLeuMetLeuAlaTyrAlaCysValThrMetLeuArgTrpAs 	84 SPASPIIeLeuHisalaPheSerGluValSerAlaAlaArgValValGly	67 uProGluAsnAlaSerGlnGlnIleHisAlaPheSerSerThrThrLeuA 	51 ValLeuGlnAlaTrpGlnArgArgPheValGlnLeuAlaGlnGluAlaL 	34 19AspTyrGlnThTHisAspIleGlyTrpSerGluGluGlnAlaSerT 	117 nSerThrPheLeuLeuMetSerProArgGlnLeuTyrGluHisPheArg 	301 GlyMetAlaArgAspProGlnGlyGluLeuLeuArgAlaGluAlaLeuG 	284 isGlyPheSerHisLysPheMetHisTrpGlnGluGluLeuLeuLeuGL 	267 sHisserargGlnAlaProAsnValAlaHisGluLeuSerGlyGlyGys 		34 heArgGluLeuLeuAspLysAlaGlnValGlyGlnAlaTyrValGlyAr {	117 pProGluGlnLeuLeuGluGluLeuGlyPropheAlaSerLeuGluGly	01 GlySerAlaTyrLeuProGlyArgProAspIleGlnTrpThrAsnLe 	.84 allleLeuThrProLeuAspCysPheTrpGluGlyAlaLysLeuGlnG 	67 ulleGluAsnGlyMetIleGluArgMetIleGluLysLeuPheProCys 	51 GlyLysSerTrpAspLeuAsnLysIleCysTyrLysSerGlyValPro: 	

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GlnGlyGlyPheAs CAGGGTGGCTTTGA sGlnArgPheSerS	LeuAlaLeuTh	laProLeuLeuLe 	AspLeuLeuGly(rGlnHisVal	IleGlnIleLeup	tLeuValPhePro	letAlaAlaPheLe	roPheLeuAlaL
spTyrAla 75 \CTACGCC 24 SerLeuLy 76	Aspvalva 71	uGlnSerH 6 CCAGTCAC 2 CCAGTCAC 7 SCCTGAGC 2	SinGluGlu 6	ThrileLe	roglngluL	AlaileLeu CCATCCTC LeuCysCy 	SUMETALAAL	euGly11eG1 TGGGAATCGG AlaLeuProG GCTCTGCCTG GCTCTGCTGCTG GThrGlyThr
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LENGTH: 1203
TYPE: PRT
ORGANISM: Homo sapiens
US-09-293-505-2
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APPLICANT: Carpenter, David A.
ITILE OF INVENTION: Patched-2
FILE REFERENCE: P1405R1
CURRENT APPLICATION NUMBER: US/09/293,505
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: US 60/081,884
EARLIER FILING DATE: 1998-04-15
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US-09-293-505-2
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361 QLAQEALPENASQQIHAFSSTTLDDILHAFSEVSAARVVGGYLLMLAYACVTMLRWDCAQ 420
                   121 QEGENILTPEALGLHLQAALTASKVQVSLYGKSWDLNKICYKSGVPLIENGMIEWMIEKL 180
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US-08-656-055-2
US-08-954-668-2
PCT-US95-13233-2
US-08-659-785-4
US-08-127-499a-1
US-08-445-640-2
US-08-445-640-2
US-08-447-314-2
US-08-445-645-2
US-08-445-6305a-1
US-08-441-104a-1
US-08-441-104a-1
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US-09-207-857-2
Sequence 2, Application US/09207857
Sequence 2, Application US/09207857
Patent No. 6309879
GENERAL INFORMATION:
GENERAL SHORTON: Bumcroft, David A.
APPLICANT: Bumcroft, David A.
TITLE OF INVENTION: HUMAN PATCHED GENES AND PROTEINS, AND USES RELATED
TITLE OF INVENTION: THERETO
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                CURRENT APPLICATION NUMBER: US/09/207,857
CURRENT FILING DATE: 1998-12-08
NUMBER OF SEO ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 2
LENGTH: 1203
                                                                          FILE REFERENCE: ONV-05001
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